

P2 14: Animal Health crisis in the Indian Ocean: Foot and mouth disease virus in Mauritius and Rodrigues in 2016

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Foot-and-mouth disease (FMD) is a contagious viral animal disease affecting domestic and wild artiodactyls (cattle, pigs, goats, pigs, African buffaloes ...). This disease is widespread throughout the world and is endemic in parts of Asia, Africa, the Middle East and South America. It is more rarely found in islands. The causative agent is a virus of the genus *Aphtovirus* within the *Picornaviridae* family and termed FMDV (Foot-and-Mouth Disease Virus). This virus has significant genetic and antigenic variability with seven immunologically distinct serotypes (O, A, C, Asia 1, SAT 1 to 3) each subdivided into several subtypes. In July-August 2016, an outbreak of FMD was reported in southeastern Africa on the Mauritius and Rodrigues Islands. Upon request, the National Reference Laboratory (NRL) in Maisons-Alfort implemented an emergency diagnosis aiming at detecting and characterizing the virus involved in this epizootic without delay. Epithelium, blood and serum samples collected from 10 bovines at Valley des Pretres and Cité la Cure in Mauritius and 3 epitheliums collected in Rodrigues were sent to the NRL. The following analyzes were performed on epithelial samples: (i) viral genome detection by real-time RT-PCR targeting the FMDV IRES region or the FMDV 3D polymerase coding region, (ii) typing by conventional RT-PCR targeting the VP1 coding region for serotypes O, A, SAT1 and SAT2, (iii) viral isolation using two epithelial cell lines (IBRS-2 and ZZ-R 127). Antigen-capture ELISA was performed on isolated virus to confirm the serotype involved and amplification then sequencing of the coding region for capsid major protein VP1 was carried out to characterize more precisely the strain involved.

FMDV was detected by RT-PCR in the 13 epithelium samples tested and successfully isolated from 11 out of the 13. The serotype was identified as FMDV-O in Ag-ELISA for all isolates and conventional RT-PCR VP1 sequencing confirmed serotype O. These results were obtained and transmitted in less than 24h after sample reception by the NRL. Finally, a comparative analysis of the VP1 sequences with the sequences available in the GenBank database showed homology with O-type sequences belonging to the ME-SA topotype Ind-2001d lineage. Overall these results enabled a precise identification of the FMDV strain involved and guided the choice of the appropriate vaccine to stop its spread.